

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A plant or yeast eukaryotic cell that comprises a prokaryotic recombinase polypeptide or a nucleic acid that encodes ~~the~~ a prokaryotic recombinase, wherein the recombinase is capable of mediating ~~can mediate~~ site-specific recombination in the eukaryotic cell between an *attB* a first recombination site and an *attP* a second recombination site to form an *attL* and an *attR* site; ~~that can serve as a substrate for recombination with the first recombination site, but in the absence of an additional factor that is not present in the eukaryotic cell; and wherein the recombinase is not capable of mediating in the eukaryotic cell cannot mediate recombination between the *attL* site and the *attR* site; two hybrid recombinase recombination sites that are formed upon recombination between the first recombination site and the second recombination site;~~

Claim 2 (original): The eukaryotic cell of claim 1, wherein the recombinase is selected from the group consisting of a bacteriophage Φ C31 integrase, a coliphage P4 recombinase, a Listeria phage recombinase, a bacteriophage R4 Sre recombinase, a CsaA recombinase, an XisF recombinase, and a transposon Tn4451 TnpX recombinase.

Claim 3 (original): The eukaryotic cell of claim 1, wherein the recombinase is a bacteriophage Φ C31 integrase.

Claim 4 (canceled).

Claim 5 (canceled).

Claim 6 (currently amended): The eukaryotic cell of claim 1, wherein the cell comprises a nucleic acid that comprises a coding sequence for the ~~an~~ recombinase polypeptide,

which coding sequence is operably linked to a promoter that mediates expression of the recombinase-encoding polynucleotide in the eukaryotic cell.

Claim 7 (original): The eukaryotic cell of claim 6, wherein the nucleic acid further comprises a selectable marker.

Claim 8 (original): The eukaryotic cell of claim 6, wherein the promoter is an inducible or a repressible promoter.

Claim 9 (currently amended): The eukaryotic cell of claim 6, wherein the nucleic acid encodes Φ C31 integrase, wherein the nucleic acid is the plasmid pLT43.

Claim 10 (currently amended): The eukaryotic cell of claim 1, wherein the cell is a yeast cell, eukaryotic cell is selected from the group consisting of an animal cell, a plant cell, a yeast cell, an insect cell and a fungal cell.

Claim 11 (currently amended): The eukaryotic cell of claim 1[[10]], wherein the eukaryotic cell is a plant cell, eukaryotic cell is a mammalian cell.

Claim 12 (currently amended): The eukaryotic cell of claim 11[[10]], wherein the eukaryotic cell is present in a plant, multicellular organism.

Claims 13 to 35. (canceled).

Claim 36 (currently amended): A plant or yeast eukaryotic cell that comprises a first bacteriophage Φ C31 recombination site;

an attP or attB recombination site of bacteriophage Φ C31 integrase integrated in its genome; and

a non-genomic nucleic acid comprising a heterologous nucleic acid or a transgene, and an attP site if the cell has the genomic attB site or an attB site if the cell has the genomic attP site.

Claim 37 (currently amended). The eukaryotic cell of claim 36, wherein the non-genomic nucleic acid comprises the transgene. recombination site is selected from the group consisting of attP and attB.

Claim 38 (currently amended): The eukaryotic cell of claim 36, wherein the eukaryotic cell further comprises ~~a second polynucleotide that comprises a second Φ C31 recombination site that undergoes recombination with the first Φ C31 recombination site when contacted with a Φ C31 integrase polypeptide.~~

Claims 39 to 42 (canceled).

Claim 43 (original): The eukaryotic cell of claim 36, wherein the eukaryotic cell further comprises a nucleic acid that comprises a polynucleotide that encodes a Φ C31 integrase polypeptide.

Claim 44 (original). The eukaryotic cell of claim 43, wherein the nucleic acid further comprises a selectable marker.

Claim 45 (original): The eukaryotic cell of claim 43, wherein the nucleic acid further comprises a promoter which results in expression of the Φ C31 integrase-encoding polynucleotide in the cell.

Claim 46 (original): The eukaryotic cell of claim 45, wherein the promoter is an inducible promoter.

Claim 47 (currently amended): The eukaryotic cell of claim 36, wherein the plant is a dicot or a monocot. eukaryotic cell is selected from the group consisting of a yeast cell, a fungal cell, a plant cell, and an animal cell.

Claim 48 (new): The cell of claim 1, wherein the cell further comprises a heterologous nucleic acid or transgene located between an *attR* recombination site and an *attL*

recombination site, wherein the heterologous nucleic acid or the transgene is stably integrated into the genome of the cell.

Claim 49 (new): The cell of claim 48, wherein the transgene is located between the *attR* recombination site and the *attL* recombination site and is stably integrated into the genome of the cell.

Claim 50 (new): The cell of claim 2, wherein the cell further comprises a heterologous nucleic acid or transgene located between an *attR* recombination site and an *attL* recombination site, wherein said heterologous nucleic acid or transgene is stably integrated into the genome of the cell.

Claim 51 (new): The cell of claim 50, wherein the transgene is located between the *attR* recombination site and the *attL* recombination site and is stably integrated into the genome of the cell.

Claim 52 (new): A eukaryotic cell in culture:
comprising an *attP* or *attB* recombination site integrated in its genome;
a non-genomic nucleic acid comprising a transgene or a heterologous nucleic acid
and an *attP* site if the cell has the genomic *attB* site or an *attP* site if the cell has the genomic *attB* site.

Claim 53 (new): A eukaryotic cell in culture comprising:
a prokaryotic recombinase polypeptide or a nucleic acid that encodes the
prokaryotic recombinase, wherein the recombinase is capable of mediating site-specific
recombination in the eukaryotic cell between an *attB* recombination site and an *attP*
recombination site to form an *attL* and an *attR* site, and is not capable of mediating in the
eukaryotic cell recombination between the *attL* site and the *attR* site; and
a heterologous nucleic acid or transgene located between the *attR* recombination
site and the *attL* recombination site, wherein said heterologous nucleic acid or transgene is stably
integrated into the genome of the cell.

Claim 54 (new): The eukaryotic cell of claim 53, wherein the eukaryotic cell is selected from the group consisting of an animal cell, a plant cell, a yeast cell, an insect cell and a fungal cell.

Claim 55 (new): The eukaryotic cell of claim 53, wherein the eukaryotic cell is a mammalian cell.

Claim 56 (new). The eukaryotic cell of claim 53, wherein the recombinase is selected from the group consisting of a bacteriophage Φ C31 integrase, a coliphage P4 recombinase, a Listeria phage recombinase, a bacteriophage R4 Sre recombinase, a CisA recombinase, an XisF recombinase, and a transposon Tn4451 TnpX recombinase.

Claim 57 (new): The eukaryotic cell of claim 56, wherein the recombinase is a bacteriophage Φ C31 integrase.

Claim 58 (new): The eukaryotic cell of claim 53, wherein the cell is a non-human cell.

Claim 59 (new): The eukaryotic cell of claim 53, wherein the cell is an embryonic stem cell.

Claim 60 (new): The eukaryotic cell of claim 53, wherein the transgene is located between the *attR* recombination site and the *attL* recombination site and is stably integrated into the genome of the cell.

Claim 61 (new): A method for obtaining site-specific recombination in a eukaryotic cell, the method comprising:

providing a eukaryotic cell that comprises an *attB* recombination site and an *attP* recombination site;

contacting the *attB* and the *attP* recombination sites with a prokaryotic recombinase polypeptide, resulting in recombination between the recombination sites, thereby forming an *attR* and an *attL* recombination site;

wherein the recombinase polypeptide can mediate site-specific recombination between the *attB* and *attP* recombination sites, but cannot mediate recombination between the *attR* and *attL* recombination sites.

Claim 62 (new): The method of claim 61, wherein the eukaryotic cell is selected from the group consisting of a yeast cell, a fungal cell, a plant cell, an insect cell and an animal cell.

Claim 63 (new): The method of claim 61, wherein the *attB* recombination site is present in a chromosome of the eukaryotic cell.

Claim 64 (new): The method of claim 63, wherein the *attP* recombination site is present in a second chromosome of the eukaryotic cell and contacting the *attB* and *attP* recombination sites with the recombinase results in translocation of chromosome arms.

Claim 65 (new): The method of claim 61, wherein the *attB* recombination site and the *attP* recombination site are present on a single nucleic acid molecule.

Claim 66 (new): The method of claim 65, wherein the *attB* recombination site and the *attP* recombination site are in a direct orientation.

Claim 67 (new): The method of claim 66, wherein the recombination results in excision of the portion of the nucleic acid molecule that lies between the *attB* and *attP* recombination sites.

Claim 68 (new): The method of claim 65, wherein the *attB* recombination site and the *attP* recombination site are in an inverted orientation.

Claim 69 (new): The method of claim 68, wherein the recombination results in inversion of the portion of the nucleic acid molecule that lies between the *attB* and *attP* recombination sites.

Claim 70 (new): The method of claim 61, wherein the eukaryotic cell comprises a polynucleotide that encodes the recombinase polypeptide.

Claim 71 (new): The method of claim 61, wherein the *attB* site is on a first linear DNA fragment and the *attP* site is on a second linear DNA fragment and contacting the *attB* and *attP* sites with the recombinase results in a translocation between the first and second linear DNA fragments.